GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 21, 2004, 10:27:03 ; Search time 387 Seconds
(without alignments)
498.380 Million cell updates/sec

Title: US-09-701-747A-2
Perfect score: 2892
Sequence: 1 MPIEIVCKIKFAEEDAKPKE.....LPNHHHPHGPPGSLFENFAC 539

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2811	97.2	539	10	US-09-772-180A-8	Sequence 8, Appli
2	2811	97.2	539	14	US-10-295-027-290	Sequence 290, App
3	2799	96.8	539	10	US-09-772-180A-2	Sequence 2, Appli
4	2571	88.9	587	10	US-09-772-180A-4	Sequence 4, Appli
5	1275	44.1	526	9	US-09-983-204-13	Sequence 13, Appl
6	1261	43.6	514	15	US-10-092-900A-104	Sequence 104, App
7	1236	42.7	574	16	US-10-789-241-18	Sequence 18, Appl
8	1236	42.7	574	17	US-10-757-262-134	Sequence 134, App
9	1198	41.4	533	14	US-10-258-073-8	Sequence 8, Appli
10	1179	40.8	512	9	US-09-983-204-14	Sequence 14, Appl
11	1179	40.8	512	14	US-10-258-073-2	Sequence 2, Appli
12	1179	40.8	512	14	US-10-258-073-6	Sequence 6, Appli
13	1179	40.8	512	17	US-10-757-262-122	Sequence 122, App
14	1170	40.5	531	14	US-10-258-073-4	Sequence 4, Appli
15	1165.5	40.3	531	14	US-10-345-680-56	Sequence 56, Appl
16	1165.5	40.3	531	14	US-10-366-288-44	Sequence 44, Appl
17	1165.5	40.3	549	9	US-09-983-204-6	Sequence 6, Appli
18	1165	40.3	543	9	US-09-983-204-2	Sequence 2, Appli
19	1139.5	39.4	518	9	US-09-983-204-4	Sequence 4, Appli
20	510	17.6	150	9	US-09-860-670-108	Sequence 108, App
21	510	17.6	150	14	US-10-227-646-108	Sequence 108, App
22	466	16.1	103	10	US-09-772-180A-6	Sequence 6, Appli
23	416	14.4	704	14	US-10-104-047-3501	Sequence 3501, Ap
24	413	14.3	669	9	US-09-983-204-15	Sequence 15, Appl
25	413	14.3	669	13	US-10-133-157-4	Sequence 4, Appli
26	413	14.3	669	14	US-10-097-340-278	Sequence 278, App
27	413	14.3	669	14	US-10-097-340-280	Sequence 280, App
28	413	14.3	669	15	US-10-373-801-28	Sequence 28, Appl
29	413	14.3	669	15	US-10-133-573-4	Sequence 4, Appli
30	413	14.3	669	16	US-10-741-601-466	Sequence 466, App
31	410	14.2	638	9	US-09-983-204-18	Sequence 18, Appl
32	410	14.2	638	13	US-10-133-157-8	Sequence 8, Appli
33	410	14.2	638	15	US-10-133-573-8	Sequence 8, Appli
34	401.5	13.9	640	13	US-10-133-157-5	Sequence 5, Appli
35	401.5	13.9	640	15	US-10-133-573-5	Sequence 5, Appli
36	397.5	13.7	640	9	US-09-983-204-16	Sequence 16, Appl
37	362	12.5	649	13	US-10-133-157-6	Sequence 6, Appli
38	362	12.5	649	15	US-10-133-573-6	Sequence 6, Appli
39	349	12.1	649	9	US-09-983-204-17	Sequence 17, Appl
40	316	10.9	515	9	US-09-983-204-19	Sequence 19, Appl
41	287	9.9	374	14	US-10-104-047-3578	Sequence 3578, Ap
42	252	8.7	555	14	US-10-168-651-27	Sequence 27, Appl
43	229.5	7.9	907	14	US-10-369-493-6677	Sequence 6677, Ap
44	176.5	6.1	114	14	US-10-106-698-6921	Sequence 6921, Ap
45	155.5	5.4	46	15	US-10-276-774-1604	Sequence 1604, Ap

ALIGNMENTS

RESULT 1
US-09-772-180A-8
; Sequence 8, Application US/09772180A
; Publication No. US20030027749A1
; GENERAL INFORMATION:
; APPLICANT: David C. Harrison
; APPLICANT: John Davis
; APPLICANT: Sharon Bingham
; APPLICANT: Trudy R. Doe
; APPLICANT: Simon Topp
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30021-C1
; CURRENT APPLICATION NUMBER: US/09/772,180A
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 09/063,848
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 9708936.1
; PRIOR FILING DATE: 1997-05-01
; PRIOR APPLICATION NUMBER: 97310289.0
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 9803566.0
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 539
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-772-180A-8

Query Match 97.2%; Score 2811; DB 10; Length 539;
Best Local Similarity 97.0%; Pred. No. 2.4e-258;
Matches 523; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MPIEIVCKIKFAEEDAKPKEKEAGDEQSLLGAAQGPAAPRDLATFASTSTLHGLGRACGP 60

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 21, 2004, 09:55:38 ; Search time 24 Seconds
(without alignments)
1489.392 Million cell updates/sec

Title: US-09-701-747A-2
Perfect score: 2892
Sequence: 1 MPIEIVCKIKFAEEDAKPKE.....LPNHHHPHGPPGSLFENFAC 539

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2814	97.3	539	4	US-09-518-959-9	Sequence 9, Appli
2	2811	97.2	539	4	US-09-518-959-8	Sequence 8, Appli
3	1323	45.7	559	3	US-09-360-197-8	Sequence 8, Appli
4	1275	44.1	526	3	US-09-360-197-2	Sequence 2, Appli
5	1249.5	43.2	514	3	US-09-360-197-4	Sequence 4, Appli
6	1198	41.4	533	3	US-09-360-197-10	Sequence 10, Appl
7	1179	40.8	512	2	US-08-828-596-2	Sequence 2, Appli
8	1179	40.8	512	3	US-09-360-197-6	Sequence 6, Appli
9	1165.5	40.3	531	3	US-09-360-197-14	Sequence 14, Appl
10	1132.5	39.2	563	3	US-09-360-197-12	Sequence 12, Appl
11	413	14.3	702	4	US-09-917-254-94	Sequence 94, Appl
12	409.5	14.2	564	3	US-09-360-197-16	Sequence 16, Appl
13	409	14.1	698	1	US-08-376-362A-20	Sequence 20, Appl
14	408.5	14.1	625	3	US-09-360-197-15	Sequence 15, Appl
15	350	12.1	753	3	US-07-861-458C-98	Sequence 98, Appl
16	347	12.0	493	6	5196333-4	Patent No. 5196333
17	330	11.4	755	3	US-07-861-458C-99	Sequence 99, Appl
18	317.5	11.0	520	3	US-07-861-458C-100	Sequence 100, App
19	225.5	7.8	294	6	5196333-2	Patent No. 5196333
20	135	4.7	97	6	5196333-9	Patent No. 5196333
21	122.5	4.2	173	6	5196333-6	Patent No. 5196333
22	116.5	4.0	67	6	5196333-10	Patent No. 5196333
23	113	3.9	1596	4	US-09-538-092-887	Sequence 887, App
24	110.5	3.8	1495	4	US-08-522-726B-1	Sequence 1, Appli
25	110.5	3.8	1495	4	US-09-337-384-1	Sequence 1, Appli
26	105.5	3.6	830	4	US-09-562-737-33	Sequence 33, Appl
27	105.5	3.6	4545	2	US-08-804-227C-14	Sequence 14, Appl
28	105.5	3.6	4550	2	US-08-804-227C-8	Sequence 8, Appli
29	105.5	3.6	4550	2	US-08-804-198-2	Sequence 2, Appli
30	104.5	3.6	561	4	US-09-252-991A-16726	Sequence 16726, A
31	103	3.6	3729	2	US-08-804-227C-4	Sequence 4, Appli
32	98.5	3.4	830	4	US-09-562-737-32	Sequence 32, Appl
33	98.5	3.4	1841	2	US-08-804-227C-6	Sequence 6, Appli
34	98.5	3.4	4630	4	US-09-091-609-2	Sequence 2, Appli
35	98.5	3.4	5215	3	US-09-105-537-2	Sequence 2, Appli
36	98	3.4	671	4	US-09-252-991A-19375	Sequence 19375, A
37	97.5	3.4	11877	3	US-09-105-537-6	Sequence 6, Appli
38	95	3.3	40	3	US-07-861-458C-118	Sequence 118, App
39	94.5	3.3	830	4	US-09-562-737-31	Sequence 31, Appl
40	93	3.2	404	4	US-09-252-991A-21555	Sequence 21555, A
41	92.5	3.2	326	4	US-09-270-767-43738	Sequence 43738, A
42	92.5	3.2	1096	4	US-09-252-991A-19328	Sequence 19328, A
43	92	3.2	73	6	5196333-5	Patent No. 5196333
44	92	3.2	885	1	US-08-372-892-4	Sequence 4, Appli
45	92	3.2	885	4	US-09-919-497-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-518-959-9
; Sequence 9, Application US/09518959
; Patent No. 6548270
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Erlander, Mark G
; APPLICANT: Huvar, Rene
; APPLICANT: Pyati, Jayashree
; TITLE OF INVENTION: DNA encoding human acid-sensing ion
; TITLE OF INVENTION: channel BNaC4 (ASIC4)
; FILE REFERENCE: ORT-1197
; CURRENT APPLICATION NUMBER: US/09/518,959
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-518-959-9

Query Match 97.3%; Score 2814; DB 4; Length 539;
Best Local Similarity 97.0%; Pred. No. 2.3e-284;
Matches 523; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

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Qy         61 GPHGLRRTLWVLALLTSLAAFLYQAASLARGYLTRPHLVAMDPAAPAPVAGFPAVTLCNI 120
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Qy        121 NRFRHSALSDADIFHLANLTGLPPKDRDGHRAAGLRYPEPDMVDILNRTGHQLADMLKSC 180
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Qy        241 ETNETSFEAGIRVQIHSQEEPPYIHQLGFGVSPGFQTFVSCQEQRLTYLPQPWGNCRAES 300
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Qy        301 KLREPELQGYSAYSVSACRLRCEKEAVLQRCHCRMVHMPGNETICPPNIYIECADHTLDS 360
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 21, 2004, 07:58:43 ; Search time 79 Seconds
(without alignments)
3925.657 Million cell updates/sec

Title: US-09-701-747A-2
Perfect score: 2892
Sequence: 1 MPIEIVCKIKFAEEDAKPKE.....LPNHHHPHGPPGSLFENPAC 539

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2889	99.9	539	2	Q9QYV9	Q9qyv9 rattus norv
2	2883	99.7	539	2	Q9JHS6	Q9jhs6 rattus norv
3	2865	99.1	539	2	Q7TNS7	Q7tns7 mus musculu
4	2811	97.2	539	2	Q9NQA4	Q9nqa4 homo sapien
5	2787	96.4	524	2	Q80XK4	Q80xk4 mus musculu
6	2680.5	92.7	647	2	Q96FT7	Q96ft7 homo sapien
7	1774	61.3	539	2	Q708S4	Q708s4 brachydanio
8	1774	61.3	539	2	CAE81922	Cae81922 brachydan
9	1671.5	57.8	558	2	Q708S3	Q708s3 brachydanio
10	1671.5	57.8	558	2	CAE81923	Cae81923 brachydan
11	1473	50.9	417	2	Q6PIN9	Q6pin9 homo sapien
12	1473	50.9	417	2	AAH31812	Aah31812 homo sapi
13	1327	45.9	559	2	Q91YB8	Q91yb8 rattus norv
14	1318	45.6	296	2	Q6GMS1	Q6gms1 homo sapien
15	1296	44.8	513	2	O88762	O88762 rattus norv
16	1275	44.1	526	1	BNA2_RAT	P55926 rattus norv
17	1274	44.1	526	2	Q6NXK8	Q6nxk8 mus musculu
18	1274	44.1	526	2	AAH67025	Aah67025 mus muscu
19	1244.5	43.0	522	2	Q7T1N4	Q7t1n4 opsanus tau
20	1237.5	42.8	557	2	Q708S8	Q708s8 brachydanio
21	1237.5	42.8	557	2	CAE81918	Cae81918 brachydan
22	1236	42.7	574	1	BNA2_HUMAN	P78348 homo sapien
23	1232	42.6	529	2	Q708S6	Q708s6 brachydanio
24	1232	42.6	529	2	CAE81920	Cae81920 brachydan
25	1198	41.4	533	2	O35240	O35240 rattus norv
26	1181	40.8	512	1	BNA1_MOUSE	Q925h0 mus musculu
27	1179	40.8	512	1	BNA1_HUMAN	Q16515 homo sapien
28	1179	40.8	512	1	BNA1_RAT	Q62962 rattus norv
29	1171.5	40.5	501	2	Q708S7	Q708s7 brachydanio
30	1171.5	40.5	501	2	CAE81919	Cae81919 brachydan
31	1170	40.5	531	2	O75906	O75906 homo sapien
32	1165.5	40.3	531	2	Q9UER8	Q9uer8 homo sapien
33	1165.5	40.3	549	2	Q9UHC3	Q9uhc3 homo sapien
34	1165	40.3	543	2	Q9UHC4	Q9uhc4 homo sapien
35	1160	40.1	542	2	Q7T1H4	Q7t1h4 opsanus tau
36	1142.5	39.5	532	2	O60263	O60263 homo sapien
37	1132.5	39.2	563	2	O55163	O55163 rattus norv
38	1129.5	39.1	563	2	Q61203	Q61203 mus musculu
39	1128.5	39.0	533	2	Q708S5	Q708s5 brachydanio
40	1128.5	39.0	533	2	CAE81921	Cae81921 brachydan
41	1117.5	38.6	563	2	Q8N3E2	Q8n3e2 homo sapien
42	1109.5	38.4	533	2	Q7T1H3	Q7t1h3 opsanus tau
43	1083	37.4	425	2	Q99NA1	Q99na1 rattus norv
44	951	32.9	309	2	O57657	O57657 fugu rubrip
45	840.5	29.1	344	2	Q96CV2	Q96cv2 homo sapien

ALIGNMENTS

RESULT 1
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ID Q9QYV9 PRELIMINARY; PRT; 539 AA.
AC Q9QYV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SPASIC protein.
GN Name=spasic;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Akopian A.N., England S., Chen C.C., Wood J.N.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the amiloride-sensitive sodium channel
CC family.
DR EMBL; AJ242554; CAB61836.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005272; F:sodium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001873; Na+channel_ASC.
DR Pfam; PF00858; ASC; 1.
DR PRINTS; PR01078; AMINACHANNEL.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport.
SQ SEQUENCE 539 AA; 59352 MW; 2DE4838AA0547097 CRC64;

Query Match 99.9%; Score 2889; DB 2; Length 539;
Best Local Similarity 99.8%; Pred. No. 2.6e-231;
Matches 538; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GPHGLRRTLWVLALLTSLAAFLYQAASLARGYLTRPHLVAMDPAAPAPVAGFPAVTLCNI 120
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Qy        121 NRFRHSALSDADIFHLANLTGLPPKDRDGHRAAGLRYPEPDMVDILNRTGHQLADMLKSC 180
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Db        121 NRFRHSALSDADIFHLANLTGLPPKDRDGHRAAGLRYPEPDMVDILNRTGHQLADMLKSC 180

Qy        181 NFSGHHCSASNFSVVYTRYGKCYTFNADPQSSLPSRAGGMGSGLEIMLDIQQEEYLPIWR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NFSGHHCSASNFSVVYTRYGKCYTFNADPQSSLPSRAGGMGSGLEIMLDIQQEEYLPIWR 240

Qy        241 ETNETSFEAGIRVQIHSQEEPPYIHQLGFGVSPGFQTFVSCQEQRLTYLPQPWGNCRAES 300
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 21, 2004, 09:47:03 ; Search time 23 Seconds
(without alignments)
2254.819 Million cell updates/sec

Title: US-09-701-747A-2
Perfect score: 2892
Sequence: 1 MPIEIVCKIKFAEEDAKPKE.....LPNHHHPHGPPGSLFENFAC 539

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1142.5	39.5	532	2	JE0091	testis sodium chan
2	422.5	14.6	548	2	T25401	hypothetical prote
3	413	14.3	669	2	A49585	Na+ channel protei
4	410	14.2	638	2	I39196	amiloride sensitiv
5	408.5	14.1	625	2	S68434	FMRFamide-activate
6	405	14.0	699	2	S29499	sodium channel pro
7	402.5	13.9	640	2	I51915	epithelial sodium
8	397.5	13.7	650	2	A54065	sodium transport p
9	396.5	13.7	632	2	I51682	epithelial sodium
10	390.5	13.5	664	2	T20420	hypothetical prote
11	386.5	13.4	660	2	I51684	epithelial sodium
12	383	13.2	663	2	T25569	hypothetical prote
13	381.5	13.2	724	2	T25700	mechanosensory pro
14	368.5	12.7	545	2	T25429	hypothetical prote
15	363.5	12.6	638	2	S41159	sodium transport p
16	361	12.5	649	2	I64847	epithelial sodium
17	356	12.3	795	2	T34468	hypothetical prote
18	354.5	12.3	849	2	T19878	hypothetical prote
19	354.5	12.3	926	2	H88226	protein C41C4.5 [i
20	349	12.1	649	2	I38204	epithelial amilori
21	347	12.0	749	2	T29859	mechanosensory pro
22	331.5	11.5	629	2	T25571	hypothetical prote
23	329	11.4	737	2	T16737	hypothetical prote
24	327.5	11.3	638	2	T37309	flr-1 protein - Ca
25	319.5	11.0	630	2	D87739	protein T28F2.7 [i
26	319.5	11.0	630	2	T15144	hypothetical prote
27	314	10.9	608	2	T25572	hypothetical prote
28	308	10.7	643	2	T21296	hypothetical prote
29	307.5	10.6	613	2	T28952	hypothetical prote
30	269.5	9.3	611	2	T20501	hypothetical prote
31	264	9.1	978	2	T16948	hypothetical prote
32	236.5	8.2	297	2	T25652	degenerin 1 (DEG-1
33	230	8.0	599	2	T15552	hypothetical prote
34	229.5	7.9	907	2	T27317	hypothetical prote
35	203	7.0	292	2	T29233	hypothetical prote
36	190.5	6.6	606	2	JW0054	amiloride-sensitiv
37	160	5.5	384	2	T19513	hypothetical prote
38	154.5	5.3	840	2	T21333	hypothetical prote
39	113	3.9	1596	2	A35927	190K DNA-binding p
40	110.5	3.8	1495	2	S60255	transcription co-r
41	104.5	3.6	956	2	B83200	probable phosphotr
42	104.5	3.6	6260	2	T30228	polyketide synthas
43	103	3.6	1535	2	S46224	peroxidasin - frui
44	101.5	3.5	1207	1	EGHU	epidermal growth f
45	99.5	3.4	1400	1	I38185	protein-tyrosine k

ALIGNMENTS

RESULT 1
JE0091
testis sodium channel 1 - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: JE0091
R;Ishibashi, K.; Marumo, F.
Biochem. Biophys. Res. Commun. 245, 589-593, 1998
A;Title: Molecular cloning of a DEG/ENaC sodium channel cDNA from human testis.
A;Reference number: JE0091; MUID:98238685; PMID:9571199
A;Accession: JE0091
A;Molecule type: mRNA
A;Residues: 1-532 <ISH>
A;Cross-references: UNIPROT:O60263; DDBJ:AB010575; NID:g3097313; PIDN:BAA25897.1; PID:g
A;Experimental source: testis
C;Keywords: glycoprotein; mitochondrion
F;43-61,443-462/Region: hydrophobic
F;175/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.5%; Score 1142.5; DB 2; Length 532;
Best Local Similarity 45.9%; Pred. No. 2.3e-85;
Matches 247; Conservative 62; Mismatches 172; Indels 57; Gaps 12;

```
Qy         35 GPAAPR----DLATFASTSTLHGLGRACGPGPHGLRRTLWVLALLTSLAAFLYQAASLAR 90
              ||    |    |:  |||  ::||||   |||   ||| :|  |:: |:| |||| |   |
Db          6 GPEEARRQASDIRVFASNCSMHGLGHVFGPGSLSLRRGMWAAAVVLSVATFLYQVAERVR 65

Qy         91 GYLTRPHLVAMDPAAPAPVAGFPAVTLCNINRFRHSALSDADIFHLAN--LTGLPPKDRD 148
                |    | |:|       :  ||||||||||  | | |:  |: | |   | || | :
Db         66 YYREFHHQTALDERESHRLI-FPAVTLCNINPLRRSRLTPNDL-HWAGSALLGLDPAEHA 123

Qy        149 GHRAAGLRYPEP---------DMVDILNRTGHQLADMLKSCNFSGHHCSASNFSVVYTRY 199
                | | | |           ||  :  | || | |||  | | |  |.  ||: ::||
Db        124 AFLRALGRPPAPPGFMPSPTFDMAQLYARAGHSLDDMLLDCRFRGQPCGPENFTTIFTRM 183

Qy        200 GKCYTFN--ADPQSSLPSRAGGMGSGLEIMLDIQQEEYLPIWRETNETSFEAGIRVQIHS 257
              |||||||  ||    | :  ||||:||:||||:|||||||:||:  || || |||||||
Db        184 GKCYTFNSGADGAELLTTTRGGMGNGLDIMLDVQQEEYLPVWRDNEETPFEVGIRVQIHG 243

Qy        258 QEEPPYIHQLGFGVSPGFQTFVSCQEQRLTYLPQPWGNCRAES----------------K 301
              |||| | ||| |||||:|||||||:|:|::|| |||:| : |                |
Db        244 HEEPPIIDQLGLGVSPGYQTFVSCQQQQLSFLPPPWGDCSSASLNPNYEPEPSDPLGSPK 303

Qy        302 LREPELQGYSAYSVSACRLRCEKEAVLQRCHCRMVHMPGNETICPPNIYIECADHTLDSL 361
                | |          ||| ||   | ::| ||||:|||:  :| |  |  ||   :|::
Db        304 PPAPAL----PIPFMGCRLACETRYVARKCGCRMVYMPGDVPVCSPQQYKNCAHPAIDAM 359

Qy        362 GGGSEGPCFCPTPCNLTRYGKEISMVKIPNRGSARYLARKYNRNETYIRENFLVLDVPFE 421
                :  | || ||  ||| ||:|||:||:| :||:||||:|| | || || | ||:|||
Db        360 --LRKDSCACPNPCASTRYAKELSMVRIPSRAAARFLARKFNRREAYIAENVLALDIFFE 417

Qy        422 ALTSEAMEQRAAYGLSALLGDLGGQMGLFIGASILTLLEILDYIYEVSWDR-LKRVWRRP 480
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 21, 2004, 07:56:27 ; Search time 73 Seconds
(without alignments)
2648.700 Million cell updates/sec

Title: US-09-701-747A-2
Perfect score: 2892
Sequence: 1 MPIEIVCKIKFAEEDAKPKE.....LPNHHHPHGPPGSLFENFAC 539

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2892	100.0	539	3	AAY53870	Aay53870 Amino aci
2	2814	97.3	539	4	AAE10898	Aae10898 Human bra
3	2811	97.2	539	2	AAW80318	Aaw80318 Neurodege
4	2811	97.2	539	4	AAE10897	Aae10897 Human bra
5	2811	97.2	539	6	ABR58577	Abr58577 Human can
6	2811	97.2	539	7	ADN38972	Adn38972 Cancer/an
7	2811	97.2	653	5	ABP69359	Abp69359 Human pol
8	2799	96.8	539	2	AAW80315	Aaw80315 Neurodege
9	2571	88.9	587	2	AAW80316	Aaw80316 Neurodege
10	1897	65.6	401	3	AAB07750	Aab07750 A human a
11	1323	45.7	559	2	AAW68507	Aaw68507 Rat acid
12	1323	45.7	559	3	AAY69178	Aay69178 A rat aci
13	1311.5	45.3	562	6	ABP70739	Abp70739 Human pro
14	1296	44.8	513	2	AAY03186	Aay03186 Rat Acid
15	1275	44.1	526	2	AAW68504	Aaw68504 Rat acid
16	1275	44.1	526	2	AAY03188	Aay03188 Rat Acid
17	1275	44.1	526	3	AAY69175	Aay69175 A rat aci
18	1265	43.7	318	8	ADH22534	Adh22534 Human tra
19	1261	43.6	514	5	ABU65092	Abu65092 Human NOV
20	1261	43.6	514	8	ADN61835	Adn61835 Human nov
21	1249.5	43.2	514	2	AAW68505	Aaw68505 Human aci
22	1249.5	43.2	514	3	AAY69176	Aay69176 A partial
23	1198	41.4	533	2	AAW68508	Aaw68508 Rat acid
24	1198	41.4	533	3	AAY69179	Aay69179 A rat aci
25	1198	41.4	533	5	AAU10906	Aau10906 Rat acid
26	1198	41.4	533	8	ADN97426	Adn97426 Rat DRASI
27	1179	40.8	512	2	AAW68506	Aaw68506 Human aci
28	1179	40.8	512	2	AAW93420	Aaw93420 Human BNC
29	1179	40.8	512	3	AAY69177	Aay69177 A human a
30	1179	40.8	512	5	AAU10905	Aau10905 Rat acid
31	1179	40.8	512	5	AAU10903	Aau10903 Human aci
32	1179	40.8	512	7	ADD14073	Add14073 Human src
33	1179	40.8	512	8	ADK71115	Adk71115 Human aci
34	1179	40.8	512	8	ADN97420	Adn97420 Rat BNC1
35	1179	40.8	512	8	ADP43821	Adp43821 Human aci
36	1170	40.5	531	2	AAY09509	Aay09509 Human pro
37	1170	40.5	531	5	AAU10904	Aau10904 Human aci
38	1170	40.5	531	8	ADN97424	Adn97424 Human DRA
39	1165.5	40.3	529	8	ADO28595	Ado28595 Human SLN
40	1165.5	40.3	531	3	AAY69181	Aay69181 A human a
41	1165.5	40.3	531	7	AAE38601	Aae38601 Human aci
42	1165.5	40.3	531	7	ADE40465	Ade40465 Human aci
43	1165.5	40.3	549	2	AAW88252	Aaw88252 Sodium ch
44	1165	40.3	543	2	AAW88250	Aaw88250 Sodium ch
45	1139.5	39.4	518	2	AAW88251	Aaw88251 Sodium ch

ALIGNMENTS

RESULT 1
AAY53870
ID AAY53870 standard; protein; 539 AA.
XX
AC AAY53870;
XX
DT 13-MAR-2000 (first entry)
XX
DE Amino acid sequence of a H+-gated cation channel designated SPASIC.
XX
KW H+-gated cation channel; SPASIC; dorsal root ganglion; gene therapy;
KW acid sensitive cation channel; central nervous system; pain response;
KW ion channel activity; neurotransmitter release; analgesic;
KW neuromodulatory; anti-inflammatory; neurotransmitter release;
KW neuronal excitability.
XX
OS Rattus norvegicus.
XX
PN WO9963081-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-GB001743.
XX
PR 03-JUN-1998; 98GB-00011965.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Wood JN, England S, Chen CC, Akopian AN;
XX
DR WPI; 2000-086977/07.
DR N-PSDB; AAZ36802.
XX
PT Novel ion channel protein for use as an analgesic drug target and for
PT identifying novel analgesic and antiinflammatory agents.
XX
PS Claim 2; Page 51-52; 55pp; English.
XX
CC The present sequence represents a H+-gated cation channel, designated
CC SPASIC. The cDNA sequence was isolated from a rat dorsal root ganglion
CC cDNA library. The protein is an acid sensitive cation channel capable of
CC reversibly mediating rapid and sustained cation current. The channel is
CC present in dorsal root ganglion and in central nervous system tissues.
CC The SPASIC polynucleotide and polypeptide are used in influencing
CC electrophysiological and/or pharmacological properties of a cell.
CC Expression of the SPASIC gene or antisense sequences leads to an increase
CC or reduction in ion channel activity. The SPASIC gene is used in gene
CC therapy or in preparation of medicaments for gene therapy to inhibit pain

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:28:07 ; Search time 1710 Seconds
(without alignments)
8465.284 Million cell updates/sec

Title: US-09-701-747A-1
Perfect score: 2622
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaa 2622

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4093002 seqs, 2760418825 residues

Word size : 16

Total number of hits satisfying chosen parameters: 297542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80	3.1	2431	16	US-10-302-172-458	Sequence 458, App
2	80	3.1	2710	15	US-10-295-027-289	Sequence 289, App
3	80	3.1	2711	10	US-09-772-180A-1	Sequence 1, Appli
4	80	3.1	2955	10	US-09-772-180A-3	Sequence 3, Appli
5	68	2.6	462	10	US-09-918-995-481	Sequence 481, App
6	68	2.6	465	10	US-09-918-995-478	Sequence 478, App
7	68	2.6	1632	10	US-09-772-180A-7	Sequence 7, Appli
8	40	1.5	65	10	US-09-908-975-2131	Sequence 2131, Ap
c 9	30	1.1	424	11	US-09-969-034-1620	Sequence 1620, Ap
10	29	1.1	254	16	US-10-424-599-84829	Sequence 84829, A
c 11	29	1.1	396	9	US-09-825-294-20	Sequence 20, Appl
c 12	29	1.1	396	9	US-09-970-966-20	Sequence 20, Appl
c 13	29	1.1	396	10	US-09-814-353-4322	Sequence 4322, Ap
c 14	29	1.1	396	10	US-09-814-353-10626	Sequence 10626, A
c 15	29	1.1	396	15	US-10-212-677-20	Sequence 20, Appl
c 16	29	1.1	396	15	US-10-361-811-20	Sequence 20, Appl
c 17	29	1.1	396	15	US-10-369-186-20	Sequence 20, Appl
18	29	1.1	451	9	US-09-860-670-39	Sequence 39, Appl
19	29	1.1	451	15	US-10-227-646-39	Sequence 39, Appl
20	29	1.1	462	15	US-10-101-510-176	Sequence 176, App
21	29	1.1	462	15	US-10-101-510-616	Sequence 616, App
c 22	29	1.1	574	9	US-09-919-580-71	Sequence 71, Appl
c 23	29	1.1	613	11	US-09-969-034-828	Sequence 828, App
c 24	29	1.1	891	14	US-10-198-846-6156	Sequence 6156, Ap
25	29	1.1	1374	17	US-10-437-963-84556	Sequence 84556, A
26	29	1.1	1654	18	US-10-425-115-44120	Sequence 44120, A
c 27	28	1.1	39	15	US-10-219-195-28	Sequence 28, Appl
c 28	28	1.1	39	15	US-10-219-195-29	Sequence 29, Appl
c 29	28	1.1	39	15	US-10-219-195-34	Sequence 34, Appl
c 30	28	1.1	39	15	US-10-219-195-49	Sequence 49, Appl
c 31	28	1.1	41	11	US-09-876-143-867	Sequence 867, App
c 32	28	1.1	46	9	US-09-827-289-22	Sequence 22, Appl
c 33	28	1.1	46	9	US-09-827-289-26	Sequence 26, Appl
34	28	1.1	62	16	US-10-182-327-182	Sequence 182, App
35	28	1.1	64	9	US-09-983-965-42	Sequence 42, Appl
36	28	1.1	67	9	US-09-983-965-245	Sequence 245, App
37	28	1.1	70	9	US-09-925-298-396	Sequence 396, App
38	28	1.1	70	14	US-10-102-806-396	Sequence 396, App
c 39	28	1.1	75	11	US-09-876-143-414	Sequence 414, App
c 40	28	1.1	75	14	US-10-066-548-2029	
41	28	1.1	75	17	US-10-[illegible]	
c 42	28	1.1	78	14	US-10-[illegible]	
43	28	1.1	88	9	[illegible]	
44	28	1.1	88	14	[illegible]	
c 45	28	1.1	91			
c 46	28	1.1	[illegible]			
c 47	28	1.1	[illegible]			
c 48	28	1.1	[illegible]			
c 49	28	1.1	[illegible]			
c 50	28	1.1	[illegible]			
51	28	1.1	[illegible]			
c 52	28	1.1	101	[illegible]		
c 53	28	1.1	103	9	US-09-[illegible]	
c 54	28	1.1	103	14	US-10-066-548-[illegible]	
c 55	28	1.1	107	14	US-10-066-548-2206	
c 56	28	1.1	107	15	US-10-102-524-1055	Sequence 1055, App
57	28	1.1	108	9	US-09-823-101-6	Sequence 6, Appli
58	28	1.1	109	9	US-09-960-352-2566	Sequence 2566, Ap
59	28	1.1	110	10	US-09-746-783-195	Sequence 195, App
60	28	1.1	110	16	US-10-242-535A-45147	Sequence 45147, A
61	28	1.1	110	16	US-10-085-783A-45147	Sequence 45147, A
c 62	28	1.1	117	14	US-10-060-036-2750	Sequence 2750, Ap
63	28	1.1	118	16	US-10-242-535A-16946	Sequence 16946, A
64	28	1.1	118	16	US-10-085-783A-16946	Sequence 16946, A
c 65	28	1.1	119	15	US-10-102-524-229	Sequence 229, App
66	28	1.1	120	9	US-09-974-300-3749	Sequence 3749, Ap
c 67	28	1.1	121	9	US-09-983-965-4235	Sequence 4235, Ap
c 68	28	1.1	122	9	US-09-878-178-1190	Sequence 1190, Ap
c 69	28	1.1	122	13	US-10-046-935-1190	Sequence 1190, Ap
c 70	28	1.1	122	14	US-10-146-502-1190	Sequence 1190, Ap
c 71	28	1.1	123	15	US-10-102-524-240	Sequence 240, App
c 72	28	1.1	130	9	US-09-764-846-279	Sequence 279, App
c 73	28	1.1	130	9	US-09-764-846-343	Sequence 343, App
74	28	1.1	130	10	US-09-764-891-7709	Sequence 7709, Ap
75	28	1.1	130	10	US-09-764-891-9411	Sequence 9411, Ap
76	28	1.1	130	10	US-09-764-891-9814	Sequence 9814, Ap
c 77	28	1.1	130	14	US-10-091-483-279	Sequence 279, App
c 78	28	1.1	130	14	US-10-091-483-343	Sequence 343, App
79	28	1.1	130	15	US-10-205-428-955	Sequence 955, App
80	28	1.1	130	15	US-10-091-414-279	Sequence 279, App
c 81	28	1.1	131	9	US-09-864-864-164	Sequence 164, App
82	28	1.1	133	9	US-09-770-696-603	Sequence 603, App
83	28	1.1	133	16	US-10-242-535A-51549	Sequence 51549, A
84	28	1.1	133	16	US-10-085-783A-51549	Sequence 51549, A
85	28	1.1	134	16	US-10-242-535A-8012	Sequence 8012, Ap

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 03:58:12 ; Search time 151 Seconds
(without alignments)
12342.308 Million cell updates/sec

Title: US-09-701-747A-1
Perfect score: 2622
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaa 2622

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 16

Total number of hits satisfying chosen parameters: 21439

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	80	3.1	2431	4	US-09-799-451-458	Sequence 458, App
	2	80	3.1	2528	4	US-09-518-959-7	Sequence 7, Appli
	3	68	2.6	1620	4	US-09-518-959-6	Sequence 6, Appli
	4	32	1.2	50	4	US-09-518-959-1	Sequence 1, Appli
	5	31	1.2	40	4	US-09-518-959-5	Sequence 5, Appli
c	6	29	1.1	396	4	US-09-640-173-20	Sequence 20, Appl
c	7	29	1.1	396	4	US-09-713-550-20	Sequence 20, Appl
c	8	29	1.1	396	4	US-09-825-294-20	Sequence 20, Appl
c	9	29	1.1	396	4	US-09-970-966-20	Sequence 20, Appl
	10	28	1.1	44	1	US-08-664-596B-9	Sequence 9, Appli
c	11	28	1.1	46	4	US-09-827-289-22	Sequence 22, Appl
c	12	28	1.1	46	4	US-09-827-289-26	Sequence 26, Appl
c	13	28	1.1	54	2	US-08-776-944-8	Sequence 8, Appli
	14	28	1.1	55	4	US-09-621-976-11651	Sequence 11651, A
	15	28	1.1	57	4	US-09-513-999C-19821	Sequence 19821, A
	16	28	1.1	59	4	US-09-621-976-11876	Sequence 11876, A
	17	28	1.1	69	4	US-09-621-976-11887	Sequence 11887, A
	18	28	1.1	69	4	US-09-621-976-12454	Sequence 12454, A
	19	28	1.1	70	4	US-09-621-976-12440	Sequence 12440, A
	20	28	1.1	72	4	US-09-621-976-12390	Sequence 12390, A
	21	28	1.1	73	4	US-09-621-976-14698	Sequence 14698, A
	22	28	1.1	77	4	US-09-621-976-12266	Sequence 12266, A
c	23	28	1.1	81	3	US-09-014-416-57	Sequence 57, Appl
	24	28	1.1	81	4	US-09-621-976-12198	Sequence 12198, A
	25	28	1.1	81	4	US-09-621-976-13601	Sequence 13601, A
	26	28	1.1	82	4	US-09-621-976-11689	Sequence 11689, A
	27	28	1.1	82	4	US-09-621-976-11841	Sequence 11841, A
	28	28	1.1	82	4	US-09-621-976-11864	Sequence 11864, A
	29	28	1.1	82	4	US-09-621-976-11888	Sequence 11888, A
	30	28	1.1	82	4	US-09-621-976-11944	Sequence 11944, A
	31	28	1.1	82	4	US-09-621-976-11949	Sequence 11949, A
	32	28	1.1	82	4	US-09-621-976-12015	Sequence 12015, A
	33	28	1.1	82	4	US-09-621-976-12088	Sequence 12088, A
	34	28	1.1	82	4	US-09-621-976-12103	Sequence 12103, A
	35	28	1.1	82	4	US-09-621-976-12127	Sequence 12127, A
	36	28	1.1	82	4	US-09-621-976-12131	Sequence 12131, A
	37	28	1.1	82	4	US-09-621-976-12137	Sequence 12137, A
	38	28	1.1	82	4	US-09-621-976-12322	Sequence 12322, A
	39	28	1.1	82	4	US-09-621-976-12368	Sequence 12368, A
	40	28	1.1	82	4	US-09-621-976-13499	Sequence 13499, A
	41	28	1.1	82	4	US-09-621-976-13526	Sequence 13526, A
	42	28	1.1	83	4	US-09-621-976-12087	Sequence 12087, A
	43	28	1.1	83	4	US-09-621-976-12175	Sequence 12175, A
	44	28	1.1	83	4	US-09-621-976-12195	Sequence 12195, A
	45	28	1.1	83	4	US-09-621-976-12429	Sequence 12429, A
	46	28	1.1	83	4	US-09-621-976-12450	Sequence 12450, A
	47	28	1.1	84	4	US-09-621-976-11710	Sequence 11710, A
c	48	28	1.1	90	1	US-08-677-944-2	Sequence 2, Appli
	49	28	1.1	91	4	US-09-621-976-12161	Sequence 12161, A
	50	28	1.1	98	4	US-09-621-976-11744	Sequence 11744, A
	51	28	1.1	105	4	US-09-621-976-13820	Sequence 13820, A
	52	28	1.1	106	4	US-09-621-976-12079	Sequence 12079, A
	53	28	1.1	123	4	US-09-621-976-12330	Sequence 12330, A
c	54	28	1.1	127	3	US-09-014-416-59	Sequence 59, Appl
	55	28	1.1	148	4	US-09-621-976-8100	Sequence 8100, Ap
	56	28	1.1	149	4	US-09-621-976-8863	Sequence 8863, Ap
	57	28	1.1	149	4	US-09-621-976-8942	Sequence 8942, Ap
	58	28	1.1	150	4	US-09-621-976-7801	Sequence 7801, Ap
	59	28	1.1	150	4	US-09-621-976-8044	Sequence 8044, Ap
	60	28	1.1	153	4	US-09-621-976-7751	Sequence 7751, Ap
	61	28	1.1	153	4	US-09-621-976-18058	Sequence 18058, A
	62	28	1.1	154	4	US-09-621-976-7748	Sequence 7748, Ap
	63	28	1.1	159	4	US-09-621-976-8623	Sequence 8623, Ap
	64	28	1.1	159	4	US-09-621-976-8655	Sequence 8655, Ap
	65	28	1.1	160	4	US-09-621-976-18071	Sequence 18071, A
	66	28	1.1	162	4	US-09-621-976-18068	Sequence 18068, A
	67	28	1.1	164	4	US-09-621-976-8070	Sequence 8070, Ap
	68	28	1.1	166	4	US-09-621-976-8651	Sequence 8651, Ap
	69	28	1.1	170	4	US-09-621-976-19172	Sequence 19172, A
c	70	28	1.1	176	3	US-09-014-416-63	Sequence 63, Appl
	71	28	1.1	177	4	US-09-621-976-8073	Sequence 8073, Ap
	72	28	1.1	179	4	US-09-621-976-18054	Sequence 18054, A
	73	28	1.1	182	4	US-09-621-976-16234	Sequence 16234, A
c	74	28	1.1	183	3	US-09-014-416-60	Sequence 60, Appl
	75	28	1.1	183	4	US-09-621-976-13606	Sequence 13606, A
	76	28	1.1	184	3	US-09-480-921B-13	Sequence 13, Appl
	77	28	1.1	195	4	US-09-621-976-18062	Sequence 18062, A
	78	28	1.1	198	1	US-08-330-108-16	Sequence 16, Appl
	79	28	1.1	198	5	PCT-US92-10087-16	Sequence 16, Appl
c	80	28	1.1	200	3	US-09-014-416-64	Sequence 64, Appl
	81	28	1.1	203	4	US-09-621-976-16454	Sequence 16454, A
	82	28	1.1	204	4	US-09-621-976-1323	Sequence 1323, Ap
	83	28	1.1	209	4	US-09-621-976-12920	Sequence 12920, A
	84	28	1.1	221	4	US-09-621-976-13585	Sequence 13585, A
c	85	28	1.1	227	2	US-08-520-678A-28	Sequence 28, Appl
c	86	28	1.1	227	3	US-08-897-126-28	Sequence 28, Appl
	87	28	1.1	228	3	US-09-328-111-484	Sequence 484, App
	88	28	1.1	232	4	US-09-621-976-17701	Sequence 17701, A
	89	28	1.1	240	4	US-09-621-976-1324	Sequence 1324, Ap
	90	28	1.1	245	4	US-09-621-976-17945	Sequence 17945, A
	91	28	1.1	247	4	US-09-621-976-17039	Sequence 17039, A
	92	28	1.1	249	4	US-09-621-976-1322	Sequence 1322, Ap
c	93	28	1.1	253	2	US-08-520-678A-25	Sequence 25, Appl
c	94	28	1.1	253	3	US-08-897-126-25	Sequence 25, Appl
c	95	28	1.1	257	2	US-08-520-678A-24	Sequence 24, Appl
c	96	28	1.1	257	3	US-08-897-126-24	Sequence 24, Appl
c	97	28	1.1	260	2	US-08-520-678A-29	Sequence 29, Appl
c	98	28	1.1	260	3	US-08-897-126-29	Sequence 29, Appl
	99	28	1.1	261	4	US-09-621-976-17067	Sequence 17067, A
	100	28	1.1	267	4	US-09-621-976-14155	Sequence 14155, A

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 03:54:47 ; Search time 5273 Seconds
(without alignments)
18119.662 Million cell updates/sec

Title: US-09-701-747A-1
Perfect score: 2622
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaa 2622

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 16

Total number of hits satisfying chosen parameters: 2484663

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	430	16.4	464	2	BF565208	BF565208 UI-R-BO1-
2	323	12.3	405	6	CB810840	CB810840 AMGNNUC:T
3	309	11.8	391	6	CB775482	CB775482 AMGNNUC:T
4	302	11.5	384	6	CB703338	CB703338 AMGNNUC:T
5	299	11.4	435	6	CB792852	CB792852 AMGNNUC:T
6	187	7.1	451	6	CB787201	CB787201 AMGNNUC:T
7	170	6.5	473	6	CB730080	CB730080 AMGNNUC:N
8	161	6.1	799	6	CA749777	CA749777 UI-M-FD0-
9	156	5.9	480	8	BZ275617	BZ275617 CH230-355
10	152	5.8	690	5	BU709210	BU709210 UI-M-EV0-
11	152	5.8	825	4	BI731397	BI731397 603353854
12	128	4.9	633	5	BU058742	BU058742 UI-M-FR0-
13	128	4.9	724	5	BQ442411	BQ442411 UI-M-EV0-
14	127	4.8	658	2	BB621654	BB621654 BB621654
15	123	4.7	426	5	BY295044	BY295044 BY295044
16	86	3.3	400	1	AL362900	AL362900 AL362900
17	86	3.3	730	8	AZ979355	AZ979355 2M0256F06
18	82	3.1	719	8	AZ730766	AZ730766 RPCI-24-1
19	81	3.1	451	5	BY290885	BY290885 BY290885
20	80	3.1	779	5	BX345391	BX345391 BX345391
21	78	3.0	816	9	CR220242	CR220242 Forward s
c 22	72	2.7	323	2	AW530335	AW530335 UI-R-BU0-
c 23	72	2.7	337	7	CR457643	CR457643 CR457643
c 24	72	2.7	400	2	BF393596	BF393596 UI-R-CA0-
c 25	72	2.7	473	2	BF411609	BF411609 UI-R-BT1-
c 26	72	2.7	474	2	AW527475	AW527475 UI-R-BO1-
c 27	72	2.7	703	4	BM386997	BM386997 UI-R-CN1-
c 28	72	2.7	712	8	BZ195341	BZ195341 CH230-465
c 29	70	2.7	512	2	BE121356	BE121356 UI-R-CA0-
30	68	2.6	516	4	BG913294	BG913294 602811996
31	66	2.5	450	6	CA451772	CA451772 UI-M-FX0-
32	66	2.5	585	6	CB058292	CB058292 NISC_jx02
33	60	2.3	616	4	BG912088	BG912088 602809988
34	52	2.0	130	2	BB595752	BB595752 BB595752
35	44	1.7	740	4	BG911389	BG911389 602807694
36	41	1.6	1150	2	BF531115	BF531115 602072283
c 37	37	1.4	678	2	BB620134	BB620134 BB620134
38	37	1.4	833	9	CR271533	CR271533 Reverse s
39	36	1.4	528	6	CB452403	CB452403 707268 MA
40	36	1.4	528	6	CB465468	CB465468 727515 MA
41	35	1.3	206	2	BB278030	BB278030 BB278030
42	35	1.3	210	2	BB282859	BB282859 BB282859
43	35	1.3	213	2	BB418210	BB418210 BB418210
44	35	1.3	220	2	BB359289	BB359289 BB359289
45	35	1.3	241	2	BB607280	BB607280 BB607280
c 46	35	1.3	274	5	BX638893	BX638893 BX638893
47	35	1.3	275	2	BB027941	BB027941 BB027941
48	35	1.3	368	4	BI731176	BI731176 603352143
49	35	1.3	382	6	BY656489	BY656489 BY656489
50	35	1.3	433	6	BY652580	BY652580 BY652580
51	35	1.3	679	1	AV323885	AV323885 AV323885
c 52	35	1.3	759	9	AG353117	AG353117 Mus muscu
53	33	1.3	423	2	AW669129	AW669129 112310 MA
c 54	33	1.3	1019	9	CNS0107N	AL098621 Drosophil
55	32	1.2	304	6	CA335120	CA335120 NISC_lt06
56	31	1.2	127	2	AW345376	AW345376 25012 MAR
57	31	1.2	272	2	BB421805	BB421805 BB421805
58	31	1.2	359	6	CD773159	CD773159 AGENCOURT
59	31	1.2	369	4	BM531723	BM531723 fx90d12.y
60	31	1.2	397	4	BM531320	BM531320 fx85g01.y
61	31	1.2	479	5	BU173697	BU173697 AGENCOURT
62	31	1.2	483	6	CA779219	CA779219 MPL384_8_
63	31	1.2	708	4	BG913866	BG913866 602812380
64	31	1.2	722	7	CN836157	CN836157 AGENCOURT
65	31	1.2	772	6	CB320076	CB320076 AGENCOURT
c 66	31	1.2	846	7	CN154737	CN154737 941972 MA
c 67	31	1.2	1101	9	CNS00EQL	AL069526 Drosophil
68	31	1.2	1116	2	BF527059	BF527059 602039972
69	30	1.1	132	2	AW068845	AW068845 cn25e11.x
70	30	1.1	136	6	CA337176	CA337176 NISC_lv10
71	30	1.1	146	5	BU962336	BU962336 AGENCOURT
c 72	30	1.1	167	6	CA667348	CA667348 wlsu1.pk0
73	30	1.1	205	4	BM570366	BM570366 ii01a10.y
74	30	1.1	219	2	BE587065	BE587065 WHE0513_B
75	30	1.1	237	5	BU963835	BU963835 AGENCOURT
76	30	1.1	268	4	BI703515	BI703515 fs90g09.y
c 77	30	1.1	290	7	CF774275	CF774275 AG_FSL_30
78	30	1.1	292	7	CO417007	CO417007 Mdfr30l1o
79	30	1.1	296	2	AW360147	AW360147 47572 MAR
80	30	1.1	316	7	CK378527	CK378527 lai22e04.
81	30	1.1	320	7	CK402038	CK402038 AUF_IfInt
82	30	1.1	335	7	CN995507	CN995507 Mdfr3001c
83	30	1.1	373	4	BM919328	BM919328 AGENCOURT
84	30	1.1	384	7	CN042061	CN042061 nm_40h_o1
85	30	1.1	385	5	BM965797	BM965797 ko17c06.y
86	30	1.1	443	2	AW734179	AW734179 sk80f12.y
87	30	1.1	489	5	BQ284601	BQ284601 fz85b04.y
88	30	1.1	528	7	CK983788	CK983788 re29c06.y
89	30	1.1	559	7	CN047777	CN047777 V2_p14_P2
90	30	1.1	561	7	CK793206	CK793206 AGENCOURT
91	30	1.1	730	6	CA821549	CA821549 RSH04C12
92	30	1.1	804	1	AL666096	AL666096 AL666096
c 93	30	1.1	804	9	AG516356	AG516356 Mus muscu
94	30	1.1	988	6	CB197997	CB197997 AGENCOURT
c 95	30	1.1	1005	5	BQ790397	BQ790397 Mosquito-
96	30	1.1	1013	5	BU178304	BU178304 AGENCOURT
97	29	1.1	75	6	CF245533	CF245533 Fcylcold2

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 02:00:56 ; Search time 818 Seconds
(without alignments)
16826.384 Million cell updates/sec

Title: US-09-701-747A-1
Perfect score: 2622
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaa 2622

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 16

Total number of hits satisfying chosen parameters: 249225

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2622	100.0	2622	3	AAZ36802	Aaz36802 Nucleic a
	2	80	3.1	2431	6	ABZ11576	Abz11576 Human pol
	3	80	3.1	2431	12	ADM44094	Adm44094 Novel hum
	4	80	3.1	2516	3	AAA59323	Aaa59323 DNA encod
	5	80	3.1	2528	5	AAD18265	Aad18265 Human bra
	6	80	3.1	2710	10	ACC72703	Acc72703 Human can
	7	80	3.1	2710	11	ADN38971	Adn38971 Cancer/an
	8	80	3.1	2711	2	AAV68056	Aav68056 Neurodege
	9	80	3.1	2752	12	ADH22600	Adh22600 cDNA enco
	10	80	3.1	2955	2	AAV68057	Aav68057 Neurodege
	11	68	2.6	462	9	ACH13269	Ach13269 Human adu
	12	68	2.6	465	9	ACH13266	Ach13266 Human adu
	13	68	2.6	1203	3	AAA59324	Aaa59324 Coding re
	14	68	2.6	1632	2	AAV68059	Aav68059 Neurodege
	15	40	1.5	65	6	ABN29383	Abn29383 Rat splic
	16	32	1.2	50	5	AAD18260	Aad18260 Human bra
	17	31	1.2	40	5	AAD18264	Aad18264 Oligo use
c	18	30	1.1	424	6	ABQ57925	Abq57925 Human col
c	19	29	1.1	271	4	AAL14984	Aal14984 Human bre
c	20	29	1.1	313	5	ABV04496	Abv04496 Human pro
	21	29	1.1	335	5	ABV57836	Abv57836 Human pro
c	22	29	1.1	396	4	AAF94829	Aaf94829 Human ova
c	23	29	1.1	396	5	ADL36736	Adl36736 Human ova
c	24	29	1.1	396	5	ADI71580	Adi71580 Human ova
c	25	29	1.1	396	6	ABL48779	Abl48779 Ovarian c
c	26	29	1.1	396	6	ABT03096	Abt03096 Human ova
c	27	29	1.1	396	11	ADM10689	Adm10689 Human ova
c	28	29	1.1	396	12	ADJ11019	Adj11019 Represent
c	29	29	1.1	396	12	ADM43280	Adm43280 Human ova
	30	29	1.1	451	4	AAI62780	Aai62780 Human cDN
	31	29	1.1	451	5	ABA13241	Aba13241 Human ner
	32	29	1.1	462	6	ABZ35505	Abz35505 Human gen
	33	29	1.1	462	6	ABZ35064	Abz35064 Human gen
c	34	29	1.1	574	6	ABK54601	Abk54601 Human col
c	35	29	1.1	613	6	ABQ57133	Abq57133 Human col
c	36	28	1.1	41	6	ABN73932	Abn73932 Bovine em
c	37	28	1.1	45	12	ADM98336	Adm98336 Human FGB
c	38	28	1.1	46	6	AAS95732	Aas95732 Allele di
c	39	28	1.1	46	6	AAS95736	Aas95736 Allele di
	40	28	1.1	48	6	ABK30223	Abk30223 CYP2D6 ge
c	41	28	1.1	51	4	AAL30531	Aal30531 Human SNP
	42	28	1.1	51	6	ABK30191	Abk30191 CYP2D6 ge
	43	28	1.1	52	6	ABK30190	Abk30190 CYP2D6 ge
c	44	28	1.1	54	2	AAT17031	Aat17031 Human mit
c	45	28	1.1	55	12	ADM98347	Adm98347 Human LPL
	46	28	1.1	57	3	AAC15746	Aac15746 Human sec
	47	28	1.1	62	5	AAD13992	Aad13992 Deletion
	48	28	1.1	64	8	ABX50113	Abx50113 Bovine ES
c	49	28	1.1	65	12	ADM98353	Adm98353 Human NPP
c	50	28	1.1	66	10	ADF11666	Adf11666 Human SRP
c	51	28	1.1	67	6	ABX14133	Abx14133 Fluoresce
	52	28	1.1	67	8	ABX50316	Abx50316 Bovine ES
	53	28	1.1	70	3	AAF22009	Aaf22009 Human bre
c	54	28	1.1	75	6	ABN73475	Abn73475 Bovine em
c	55	28	1.1	78	6	ABV96830	Abv96830 Human pan
	56	28	1.1	83	3	AAF22006	Aaf22006 Human bre
c	57	28	1.1	84	12	ADK52282	Adk52282 Murine ty
c	58	28	1.1	85	12	ADG65306	Adg65306 Template
	59	28	1.1	87	6	ABA99435	Aba99435 B. mori T
	60	28	1.1	89	8	ABX44974	Abx44974 Bovine ES
c	61	28	1.1	90	2	AAT47082	Aat47082 Synthetic
c	62	28	1.1	101	6	ABL37986	Abl37986 Human col
c	63	28	1.1	101	6	ADG19100	Adg19100 RNA-depen
	64	28	1.1	103	10	ADC17856	Adc17856 Monobacta
	65	28	1.1	107	10	ADC17845	Adc17845 Monobacta
	66	28	1.1	108	4	AAH43640	Aah43640 SSG #6. 1
c	67	28	1.1	109	5	AAF98681	Aaf98681 Human ova
	68	28	1.1	109	8	ABX37401	Abx37401 Bovine ES
	69	28	1.1	110	2	AAX35561	Aax35561 Secreted
	70	28	1.1	110	9	ADA45152	Ada45152 Human pol
	71	28	1.1	111	10	ADC17844	Adc17844 Monobacta
	72	28	1.1	111	10	ADG37675	Adg37675 Aspergill
	73	28	1.1	112	10	ADC17848	Adc17848 Monobacta
	74	28	1.1	114	10	ADC17852	Adc17852 Monobacta
	75	28	1.1	115	6	ABA82937	Aba82937 Human pro
c	76	28	1.1	116	4	AAL19706	Aal19706 Human bre
c	77	28	1.1	117	6	ABV97342	Abv97342 Human pan
	78	28	1.1	120	3	AAA89576	Aaa89576 Exo20 nuc
c	79	28	1.1	120	4	AAH70046	Aah70046 Human cer
	80	28	1.1	120	6	ABK76458	Abk76458 Bacillus
c	81	28	1.1	121	8	ABX54306	Abx54306 Bovine ES
	82	28	1.1	122	12	ADO41190	Ado41190 Human cDN
c	83	28	1.1	125	6	ABL37601	Abl37601 Human col
c	84	28	1.1	127	2	AAX24845	Aax24845 Infectiou
	85	28	1.1	130	4	AAK89973	Aak89973 Human dig
	86	28	1.1	130	4	AAI62629	Aai62629 Human bre
	87	28	1.1	130	4	AAK78760	Aak78760 Human imm
	88	28	1.1	130	4	AAK79573	Aak79573 Human imm
	89	28	1.1	130	4	AAK73943	Aak73943 Human imm
	90	28	1.1	130	4	AAL06723	Aal06723 Human rep
	91	28	1.1	130	4	AAL05021	Aal05021 Human rep
	92	28	1.1	130	4	AAL07126	Aal07126 Human rep
	93	28	1.1	130	4	ABA08160	Aba08160 Human ova
	94	28	1.1	130	4	ABL97914	Abl97914 Human tes

OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 02:03:42 ; Search time 7228 Seconds
(without alignments)
17154.620 Million cell updates/sec

Title: US-09-701-747A-1
Perfect score: 2622
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaa 2622

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 16

Total number of hits satisfying chosen parameters: 478857

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2622	100.0	2622	6	AX009297	AX009297 Sequence
	2	2195	83.7	2622	10	RNO242554	AJ242554 Rattus no
	3	1761	67.2	2532	10	RNO271642	AJ271642 Rattus no
c	4	823	31.4	216648	10	AC112361	AC112361 Rattus no
	5	823	31.4	266167	2	AC121633	AC121633 Rattus no
	6	161	6.1	2301	10	BC046481	BC046481 Mus muscu
	7	161	6.1	2478	10	BC055772	BC055772 Mus muscu
	8	137	5.2	177632	2	AC114651	AC114651 Mus muscu
c	9	137	5.2	197109	2	AC115011	AC115011 Mus muscu
	10	80	3.1	744	9	HSA408881	AJ408881 Homo sapi
	11	80	3.1	2528	6	AR306271	AR306271 Sequence
	12	80	3.1	2697	9	BC010439	BC010439 Homo sapi
	13	80	3.1	2711	6	E31843	E31843 Novel compo
	14	80	3.1	2711	6	AX002412	AX002412 Sequence
	15	80	3.1	2955	6	E31844	E31844 Novel compo
	16	80	3.1	2955	6	AX002414	AX002414 Sequence
	17	80	3.1	3345	9	BC031812	BC031812 Homo sapi
	18	80	3.1	3685	9	HSA271643	AJ271643 Homo sapi
	19	80	3.1	183625	9	AC053503	AC053503 Homo sapi
	20	80	3.1	184176	2	AC149120	AC149120 Papio anu
c	21	80	3.1	186883	2	AC040991	AC040991 Homo sapi
	22	80	3.1	193064	2	AC149860	AC149860 Papio anu
	23	68	2.6	1620	6	AR306270	AR306270 Sequence
	24	68	2.6	1632	6	E31846	E31846 Novel compo
	25	68	2.6	1632	6	AX002418	AX002418 Sequence
	26	68	2.6	2439	9	BC073912	BC073912 Homo sapi
	27	63	2.4	200465	2	AC148786	AC148786 Otolemur
	28	63	2.4	215101	2	AC148847	AC148847 Otolemur
	29	59	2.3	1452	6	CQ714799	CQ714799 Sequence
	30	50	1.9	1315	9	HSA408882	AJ408882 Homo sapi
	31	50	1.9	135033	9	AC009955	AC009955 Homo sapi
	32	42	1.6	53239	2	AC011971	AC011971 Homo sapi
	33	40	1.5	65	6	CQ532496	CQ532496 Sequence
	34	32	1.2	50	6	AR306265	AR306265 Sequence
	35	31	1.2	40	6	AR306269	AR306269 Sequence
	36	30	1.1	601	11	G94636	G94636 S208P6415RB
c	37	29	1.1	271	6	CQ422415	CQ422415 Sequence
c	38	29	1.1	313	6	CQ472620	CQ472620 Sequence
	39	29	1.1	335	6	CQ525988	CQ525988 Sequence
c	40	29	1.1	396	6	CQ397251	CQ397251 Sequence
c	41	29	1.1	396	6	CQ403555	CQ403555 Sequence
c	42	29	1.1	396	6	AR391197	AR391197 Sequence
c	43	29	1.1	396	6	AR392902	AR392902 Sequence
c	44	29	1.1	396	6	AR489632	AR489632 Sequence
c	45	29	1.1	396	6	AR493873	AR493873 Sequence
c	46	29	1.1	396	6	AX093202	AX093202 Sequence
c	47	29	1.1	574	6	AX381133	AX381133 Sequence
	48	29	1.1	1547	9	HSA408884	AJ408884 Homo sapi
	49	29	1.1	183793	2	CR450793	CR450793 Danio rer
	50	29	1.1	186883	2	AC040991	AC040991 Homo sapi
	51	29	1.1	190260	2	CR538726	CR538726 Danio rer
c	52	29	1.1	227369	2	AC114469	AC114469 Rattus no
	53	29	1.1	230637	2	AC095345	AC095345 Rattus no
c	54	29	1.1	246991	2	AC122956	AC122956 Rattus no
	55	29	1.1	249173	2	AC135886	AC135886 Rattus no
	56	28	1.1	44	6	AR038858	AR038858 Sequence
c	57	28	1.1	46	6	AX287579	AX287579 Sequence
c	58	28	1.1	46	6	AX287583	AX287583 Sequence
c	59	28	1.1	51	6	CQ005099	CQ005099 Sequence
c	60	28	1.1	54	6	A49113	A49113 Sequence 8
	61	28	1.1	55	6	AR420154	AR420154 Sequence
	62	28	1.1	55	6	AX980848	AX980848 Sequence
	63	28	1.1	55	6	BD115707	BD115707 EST and e
	64	28	1.1	57	6	AX903958	AX903958 Sequence
	65	28	1.1	57	6	BD039491	BD039491 Sequence
	66	28	1.1	59	6	AR420379	AR420379 Sequence
	67	28	1.1	59	6	AX981073	AX981073 Sequence
	68	28	1.1	59	6	BD115932	BD115932 EST and e
	69	28	1.1	62	6	AX205290	AX205290 Sequence
	70	28	1.1	69	6	AR420390	AR420390 Sequence
	71	28	1.1	69	6	AR420957	AR420957 Sequence
	72	28	1.1	69	6	AX981084	AX981084 Sequence
	73	28	1.1	69	6	AX981651	AX981651 Sequence
	74	28	1.1	69	6	BD115943	BD115943 EST and e
	75	28	1.1	69	6	BD116510	BD116510 EST and e
	76	28	1.1	70	6	AR420943	AR420943 Sequence
	77	28	1.1	70	6	AX981637	AX981637 Sequence
	78	28	1.1	70	6	BD116496	BD116496 EST and e
	79	28	1.1	72	6	AR420893	AR420893 Sequence
	80	28	1.1	72	6	AX981587	AX981587 Sequence
	81	28	1.1	72	6	BD116446	BD116446 EST and e
	82	28	1.1	73	6	AR423201	AR423201 Sequence
	83	28	1.1	73	6	AX983895	AX983895 Sequence
	84	28	1.1	73	6	BD118754	BD118754 EST and e
	85	28	1.1	77	6	AR420769	AR420769 Sequence
	86	28	1.1	77	6	AX981463	AX981463 Sequence
	87	28	1.1	77	6	BD116322	BD116322 EST and e
c	88	28	1.1	81	6	AR119865	AR119865 Sequence
	89	28	1.1	81	6	AR420701	AR420701 Sequence
	90	28	1.1	81	6	AR422104	AR422104 Sequence
	91	28	1.1	81	6	AX981395	AX981395 Sequence
	92	28	1.1	81	6	AX982798	AX982798 Sequence

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 00:33:06 ; Search time 908 Seconds
(without alignments)
15942.331 Million cell updates/sec

Title: US-09-701-747A-1
Perfect score: 2622
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaa 2622

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1834.2	70.0	2710	15	US-10-295-027-289	Sequence 289, App
2	1816.6	69.3	2711	10	US-09-772-180A-1	Sequence 1, Appli
3	1717	65.5	2431	16	US-10-302-172-458	Sequence 458, App
4	1555	59.3	2955	10	US-09-772-180A-3	Sequence 3, Appli
5	1411.2	53.8	1632	10	US-09-772-180A-7	Sequence 7, Appli
6	463.8	17.7	1624	16	US-10-092-900A-103	Sequence 103, App
7	391.4	14.9	1732	15	US-10-258-073-3	Sequence 3, Appli
8	391.2	14.9	1596	15	US-10-345-680-57	Sequence 57, Appl
9	391.2	14.9	1650	9	US-09-983-204-5	Sequence 5, Appli
10	391.2	14.9	1723	9	US-09-983-204-1	Sequence 1, Appli
11	391.2	14.9	1746	15	US-10-345-680-55	Sequence 55, Appl
12	391.2	14.9	1746	15	US-10-366-288-43	Sequence 43, Appl
13	387.6	14.8	1711	9	US-09-983-204-3	Sequence 3, Appli
c 14	385	14.7	3918	15	US-10-101-510-421	Sequence 421, App
15	385	14.7	3923	17	US-10-283-975A-64	Sequence 64, Appl
16	385	14.7	3923	17	US-10-789-241-17	Sequence 17, Appl
17	385	14.7	3923	18	US-10-757-262-133	Sequence 133, App
18	351	13.4	1602	15	US-10-258-073-7	Sequence 7, Appli
19	335	12.8	1539	9	US-09-954-456-750	Sequence 750, App
20	335	12.8	1539	16	US-10-305-720-1102	Sequence 1102, Ap
21	335	12.8	1663	18	US-10-757-262-121	Sequence 121, App
22	335	12.8	2565	15	US-10-258-073-5	Sequence 5, Appli
23	335	12.8	2748	15	US-10-258-073-1	Sequence 1, Appli
24	332.8	12.7	462	15	US-10-101-510-176	Sequence 176, App
25	332.8	12.7	462	15	US-10-101-510-616	Sequence 616, App
26	318.6	12.2	451	9	US-09-860-670-39	Sequence 39, Appl
27	318.6	12.2	451	15	US-10-227-646-39	Sequence 39, Appl
28	309.6	11.8	397	9	US-09-960-352-1490	Sequence 1490, Ap
29	300.6	11.5	465	10	US-09-918-995-478	Sequence 478, App
30	299.4	11.4	462	10	US-09-918-995-481	Sequence 481, App
31	263	10.0	508	10	US-09-772-180A-5	Sequence 5, Appli
32	191.2	7.3	831	13	US-10-027-632-155396	Sequence 155396,
33	191.2	7.3	831	15	US-10-027-632-155396	Sequence 155396,
34	173.6	6.6	393	16	US-10-305-720-206	Sequence 206, App
35	115.2	4.4	425	9	US-09-960-352-10001	Sequence 10001, A
36	114.2	4.4	458	10	US-09-918-995-28399	Sequence 28399, A
37	112.2	4.3	358	9	US-09-728-445-590	Sequence 590, App
38	80.6	3.1	354	15	US-10-106-698-2644	Sequence 2644, Ap
c 39	75.8	2.9	438	16	US-10-276-774-254	Sequence 254, App
40	64	2.4	65	10	US-09-908-975-2131	Sequence 2131, Ap
41	63.6	2.4	343	17	US-10-283-975A-116	Sequence 116, App
42	50.8	1.9	459	10	US-09-918-995-2809	Sequence 2809, Ap
43	50	1.9	2931	13	US-10-027-632-111727	Sequence 111727,
44	50	1.9	2931	15	US-10-027-632-111727	Sequence 111727,
c 45	46.8	1.8	653	17	US-10-437-963-94593	Sequence 94593, A

ALIGNMENTS

RESULT 1
US-10-295-027-289
; Sequence 289, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 21:43:21 ; Search time 151 Seconds
(without alignments)
12342.308 Million cell updates/sec

Title: US-09-701-747A-1
Perfect score: 2622
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaaa 2622

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1748	66.7	2528	4	US-09-518-959-7	Sequence 7, Appli
	2	1717	65.5	2431	4	US-09-799-451-458	Sequence 458, App
	3	1400.8	53.4	1620	4	US-09-518-959-6	Sequence 6, Appli
	4	491.2	18.7	3647	3	US-09-360-197-7	Sequence 7, Appli
	5	440.2	16.8	1620	3	US-09-360-197-3	Sequence 3, Appli
	6	415	15.8	3562	3	US-09-360-197-1	Sequence 1, Appli
	7	391.2	14.9	1736	3	US-09-360-197-13	Sequence 13, Appl
	8	351	13.4	1602	3	US-09-360-197-9	Sequence 9, Appli
	9	347.2	13.2	1948	3	US-09-360-197-11	Sequence 11, Appl
	10	335	12.8	1539	2	US-08-828-596-1	Sequence 1, Appli
	11	335	12.8	1539	4	US-09-016-434-1102	Sequence 1102, Ap
	12	335	12.8	1666	3	US-09-360-197-5	Sequence 5, Appli
	13	173.6	6.6	393	4	US-09-016-434-206	Sequence 206, App
c	14	47.8	1.8	7218	1	US-08-232-463-14	Sequence 14, Appl
c	15	43.2	1.6	2218	2	US-08-845-998-5	Sequence 5, Appli
c	16	43.2	1.6	2218	3	US-09-206-537-5	Sequence 5, Appli
c	17	43.2	1.6	2218	3	US-09-430-854-5	Sequence 5, Appli
	18	42.8	1.6	1605	4	US-09-149-476-187	Sequence 187, App
	19	40.8	1.6	985	4	US-09-322-409-25	Sequence 25, Appl
c	20	40.8	1.6	985	4	US-09-322-409-27	Sequence 27, Appl
	21	40.8	1.6	985	4	US-09-451-527-25	Sequence 25, Appl
c	22	40.8	1.6	985	4	US-09-451-527-27	Sequence 27, Appl
	23	40.6	1.5	2639	3	US-09-374-135-1	Sequence 1, Appli
	24	40.6	1.5	7218	1	US-08-232-463-14	Sequence 14, Appl
	25	40.4	1.5	1988	2	US-08-712-948-8	Sequence 8, Appli
	26	40.4	1.5	1988	4	US-09-023-655-1218	Sequence 1218, Ap
c	27	40	1.5	2259	2	US-08-845-998-3	Sequence 3, Appli
c	28	40	1.5	2259	3	US-09-206-537-3	Sequence 3, Appli
c	29	40	1.5	2259	3	US-09-430-854-3	Sequence 3, Appli
	30	39.8	1.5	8051	2	US-08-576-626A-2	Sequence 2, Appli
c	31	39.4	1.5	636	3	US-09-385-982-317	Sequence 317, App
c	32	39.2	1.5	474	4	US-09-621-976-18033	Sequence 18033, A
	33	39.2	1.5	1013	4	US-09-322-409-6	Sequence 6, Appli
c	34	39.2	1.5	1013	4	US-09-322-409-8	Sequence 8, Appli
	35	39.2	1.5	1013	4	US-09-451-527-6	Sequence 6, Appli
c	36	39.2	1.5	1013	4	US-09-451-527-8	Sequence 8, Appli
	37	39	1.5	289	3	US-09-007-005-17	Sequence 17, Appl
	38	39	1.5	289	3	US-09-244-796-17	Sequence 17, Appl
	39	39	1.5	2806	4	US-09-653-839-9	Sequence 9, Appli
	40	39	1.5	2806	4	US-10-202-619-9	Sequence 9, Appli
	41	38.8	1.5	8100	4	US-09-554-337-4	Sequence 4, Appli
	42	38.8	1.5	11517	1	US-07-920-281C-1	Sequence 1, Appli
	43	38.8	1.5	11517	3	US-08-466-277-1	Sequence 1, Appli
	44	38.8	1.5	11517	4	US-09-688-842-1	Sequence 1, Appli
	45	38.8	1.5	15538	4	US-09-554-337-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-518-959-7
; Sequence 7, Application US/09518959
; Patent No. 6548270
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Erlander, Mark G
; APPLICANT: Huvar, Rene
; APPLICANT: Pyati, Jayashree
; TITLE OF INVENTION: DNA encoding human acid-sensing ion
; TITLE OF INVENTION: channel BNaC4 (ASIC4)
; FILE REFERENCE: ORT-1197
; CURRENT APPLICATION NUMBER: US/09/518,959
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-518-959-7

Query Match 66.7%; Score 1748; DB 4; Length 2528;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 2131; Conservative 0; Mismatches 353; Indels 49; Gaps 13;

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Db        1 ACTCCCCCACCTCGGGCCCCCACCCTGTCCCTGTCCTCTTCCCGCTTGCCCTGAGTTTAG 60

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Db       61 AAGAGCAGCCGCTGCCACCACTGCCACTCGGGAGGGCACCAGGGCTGCTGGCTAGGGAGG 120

Qy      248 GACAGTAGCAGTGAGGCTCTGGCCAGTCCCAGCAGCCGGGGACAGATGCCGATCGAGATT 307
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Qy      308 GTGTGCAAAATCAAATTTGCTGAGGAGGATGCAAAACCCAAGGAGAAGGAGGCAGGGGAT 367
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Qy      368 GAGCAGAGCCTCCTGGGGGCTGCTCAGGGGCCAGCAGCCCCTCGGGACCTGGCTACCTTT 427
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Qy      428 GCCAGCACCAGTACTCTGCATGGGCTGGGCCGGGCCTGTGGCCCAGGCCCCCATGGACTG 487
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 21:31:31 ; Search time 5273 Seconds
(without alignments)
18119.662 Million cell updates/sec

Title: US-09-701-747A-1
Perfect score: 2622
Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaa 2622

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	743.6	28.4	825	4	BI731397	BI731397 603353854
	3	695.8	26.5	724	5	BQ442411	BQ442411 UI-M-EV0-
	4	669.2	25.5	690	5	BU709210	BU709210 UI-M-EV0-
c	5	646.8	24.7	703	4	BM386997	BM386997 UI-R-CN1-
	6	641.2	24.5	779	5	BX345391	BX345391 BX345391
	7	613.8	23.4	633	5	BU058742	BU058742 UI-M-FR0-
	8	589.2	22.5	658	2	BB621654	BB621654 BB621654
	9	520.2	19.8	679	1	AV323885	AV323885 AV323885
	10	478.6	18.3	585	6	CB058292	CB058292 NISC_jx02
c	11	473	18.0	512	2	BE121356	BE121356 UI-R-CA0-
	12	463.4	17.7	740	4	BG911389	BG911389 602807694
	13	458.8	17.5	812	4	BG818664	BG818664 602778855
	14	453.8	17.3	464	2	BF565208	BF565208 UI-R-BO1-
c	15	437	16.7	473	2	BF411609	BF411609 UI-R-BT1-
c	16	436.4	16.6	474	2	AW527475	AW527475 UI-R-BO1-
	17	404.2	15.4	3830	3	BC028722	BC028722 Homo sapi
	18	401.4	15.3	513	4	BM257315	BM257315 520890 MA
	19	398	15.2	616	4	BG912088	BG912088 602809988
	20	390.4	14.9	451	5	BY290885	BY290885 BY290885
	21	381.8	14.6	426	5	BY295044	BY295044 BY295044
	22	380.2	14.5	1059	4	BG825318	BG825318 602747771
	23	372.6	14.2	940	1	AL534267	AL534267 AL534267
	24	372.4	14.2	405	6	CB810840	CB810840 AMGNNUC:T
c	25	369.8	14.1	400	2	BF393596	BF393596 UI-R-CA0-
	26	358.4	13.7	391	6	CB775482	CB775482 AMGNNUC:T
	27	358.4	13.7	400	1	AL362900	AL362900 AL362900
	28	357.6	13.6	450	6	CA451772	CA451772 UI-M-FX0-
c	29	356.6	13.6	712	8	BZ195341	BZ195341 CH230-465
	30	351.4	13.4	384	6	CB703338	CB703338 AMGNNUC:T
	31	348.4	13.3	435	6	CB792852	CB792852 AMGNNUC:T
	32	344	13.1	3470	3	HSM805478	AL834182 Homo sapi
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	34	333.2	12.7	866	7	CK238032	CK238032 AGENCOURT
	35	329.2	12.6	423	2	AW669129	AW669129 112310 MA
	36	325.8	12.4	433	6	BY652580	BY652580 BY652580
	37	320.6	12.2	483	6	CA779219	CA779219 MPL384_8_
	38	317.6	12.1	667	4	BG912912	BG912912 602807309
	39	315.4	12.0	451	6	CB787201	CB787201 AMGNNUC:T
	40	315.4	12.0	473	6	CB730080	CB730080 AMGNNUC:N
c	41	311	11.9	337	7	CR457643	CR457643 CR457643
	42	298.8	11.4	708	4	BG913866	BG913866 602812380
c	43	294.2	11.2	323	2	AW530335	AW530335 UI-R-BU0-
	44	292.8	11.2	382	6	BY656489	BY656489 BY656489
	45	274.2	10.5	1254	6	CD326863	CD326863 AGENCOURT

ALIGNMENTS

RESULT 1
CA749777
LOCUS CA749777 799 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FD0-cdg-a-19-0-UI.r1 NIH_BMAP_FD0 Mus musculus cDNA clone IMAGE:6828284 5', mRNA sequence.
ACCESSION CA749777
VERSION CA749777.1 GI:25572573
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 799)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.
FEATURES Location/Qualifiers
source 1. .799
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FD0"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 17:12:06 ; Search time 816 Seconds
(without alignments)
16867.625 Million cell updates/sec

Title: US-09-701-747A-1
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Sequence: 1 agtgacagctgtgcgggtgc.....aaaaaaaaaaaaaaaaaaa 2622

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
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2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
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7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2609	99.5	2622	3	AAZ36802	Aaz36802 Nucleic a
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3	1834.2	70.0	2710	11	ADN38971	Adn38971 Cancer/an
4	1816.6	69.3	2711	2	AAV68056	Aav68056 Neurodege
5	1748	66.7	2528	5	AAD18265	Aad18265 Human bra
6	1747.4	66.6	2752	12	ADH22600	Adh22600 cDNA enco
7	1717	65.5	2431	6	ABZ11576	Abz11576 Human pol
8	1717	65.5	2431	12	ADM44094	Adm44094 Novel hum
9	1555	59.3	2955	2	AAV68057	Aav68057 Neurodege
10	1411.2	53.8	1632	2	AAV68059	Aav68059 Neurodege
11	1199.4	45.7	2516	3	AAA59323	Aaa59323 DNA encod
12	951.8	36.3	1203	3	AAA59324	Aaa59324 Coding re
13	492.8	18.8	2962	2	AAX28161	Aax28161 Rat Acid
14	491.2	18.7	3647	2	AAV60842	Aav60842 Rat acid
15	491.2	18.7	3647	3	AAZ61200	Aaz61200 cDNA enco
16	487.2	18.6	3658	8	ABZ77869	Abz77869 Human pro
17	463.8	17.7	1624	6	ABX97059	Abx97059 Human NOV
18	463.8	17.7	1624	12	ADN61834	Adn61834 Human cDN
19	441.8	16.8	3785	9	ABQ80412	Abq80412 Human ENa
20	440.2	16.8	1620	2	AAV60840	Aav60840 Partial h
21	440.2	16.8	1620	3	AAZ61198	Aaz61198 cDNA enco
22	415	15.8	3562	2	AAV60839	Aav60839 Rat acid
23	415	15.8	3562	3	AAZ61197	Aaz61197 cDNA enco
24	391.4	14.9	1596	12	ADN97423	Adn97423 Human DRA
25	391.4	14.9	1732	2	AAX56237	Aax56237 Human pro
26	391.4	14.9	1732	6	AAS17126	Aas17126 Human cDN
27	391.2	14.9	1650	2	AAV84191	Aav84191 Sodium ch
28	391.2	14.9	1723	2	AAV84189	Aav84189 Sodium ch
29	391.2	14.9	1736	3	AAZ61203	Aaz61203 cDNA enco
30	391.2	14.9	1746	10	AAD58502	Aad58502 Human aci
31	391.2	14.9	1746	10	ADE40464	Ade40464 Human aci
32	391.2	14.9	1746	12	ADO28594	Ado28594 Human SLN
33	387.6	14.8	1711	2	AAV84190	Aav84190 Sodium ch
c 34	385	14.7	3918	6	ABZ35310	Abz35310 Human gen
35	385	14.7	3923	10	ADE84845	Ade84845 Farnesyl
36	351	13.4	1602	2	AAV60843	Aav60843 Rat acid
37	351	13.4	1602	3	AAZ61201	Aaz61201 cDNA enco
38	351	13.4	1602	6	AAS17128	Aas17128 Rat cDNA
39	351	13.4	1602	12	ADN97425	Adn97425 Rat DRASI
40	347.2	13.2	1948	2	AAV60844	Aav60844 Rat acid
41	347.2	13.2	1948	3	AAZ61202	Aaz61202 cDNA enco
42	347.2	13.2	1948	12	ADP43818	Adp43818 Rat acid-
43	344	13.1	1689	12	ADP43831	Adp43831 Human CB1
44	344	13.1	1689	12	ADP43833	Adp43833 Human SC2
45	344	13.1	1702	12	ADP43822	Adp43822 Human CB1

ALIGNMENTS

RESULT 1
AAZ36802
ID AAZ36802 standard; cDNA to mRNA; 2622 BP.
XX
AC AAZ36802;
XX
DT 13-MAR-2000 (first entry)
XX
DE Nucleic acid encoding a H+-gated cation channel designated SPASIC.
XX
KW H+-gated cation channel; SPASIC; dorsal root ganglion; gene therapy;
KW acid sensitive cation channel; central nervous system; pain response;
KW ion channel activity; neurotransmitter release; analgesic;
KW neuromodulatory; anti-inflammatory; neurotransmitter release;
KW neuronal excitability;ds.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 293. .1912
FT /*tag= a
FT /product= "H+-gated cation channel"
XX
PN WO9963081-A2.
XX
PD 09-DEC-1999.
XX
PF 03-JUN-1999; 99WO-GB001743.
XX
PR 03-JUN-1998; 98GB-00011965.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Wood JN, England S, Chen CC, Akopian AN;
XX
DR WPI; 2000-086977/07.
DR P-PSDB; AAY53870.
XX
PT Novel ion channel protein for use as an analgesic drug target and for
PT identifying novel analgesic and antiinflammatory agents.
XX
PS Claim 11; Page 48-51; 55pp; English.
XX
CC The present sequence encodes a H+-gated cation channel, designated

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 17:17:26 ; Search time 7230 Seconds
(without alignments)
17149.874 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	2211.8	84.4	2478	10	BC055772	BC055772 Mus muscu
	5	2035.8	77.6	2301	10	BC046481	BC046481 Mus muscu
	6	1816.6	69.3	2711	6	E31843	E31843 Novel compo
	7	1816.6	69.3	2711	6	AX002412	AX002412 Sequence
	8	1748	66.7	2528	6	AR306271	AR306271 Sequence
	9	1742.4	66.5	2697	9	BC010439	BC010439 Homo sapi
	10	1555	59.3	2955	6	E31844	E31844 Novel compo
	11	1555	59.3	2955	6	AX002414	AX002414 Sequence
	12	1411.2	53.8	1632	6	E31846	E31846 Novel compo
	13	1411.2	53.8	1632	6	AX002418	AX002418 Sequence
	14	1400.8	53.4	1620	6	AR306270	AR306270 Sequence
	15	1199.4	45.7	3685	9	HSA271643	AJ271643 Homo sapi
	16	1027.2	39.2	1452	6	CQ714799	CQ714799 Sequence
	17	1007.4	38.4	3345	9	BC031812	BC031812 Homo sapi
	18	873.2	33.3	266167	2	AC121633	AC121633 Rattus no
c	19	873	33.3	216648	10	AC112361	AC112361 Rattus no
	20	850.6	32.4	177632	2	AC114651	AC114651 Mus muscu
c	21	850.6	32.4	197109	2	AC115011	AC115011 Mus muscu
	22	785	29.9	215101	2	AC148847	AC148847 Otolemur
	23	783.4	29.9	200465	2	AC148786	AC148786 Otolemur
	24	782.6	29.8	184176	2	AC149120	AC149120 Papio anu
	25	782.6	29.8	193064	2	AC149860	AC149860 Papio anu
	26	773	29.5	183625	9	AC053503	AC053503 Homo sapi
	27	716.4	27.3	2439	9	BC073912	BC073912 Homo sapi
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	29	627.8	23.9	2286	5	AJ609619	AJ609619 Danio rer
	30	602.6	23.0	744	9	HSA408881	AJ408881 Homo sapi
	31	570.6	21.8	2296	5	AJ609620	AJ609620 Danio rer
	32	492.8	18.8	2962	6	A98491	A98491 Sequence 1
	33	492.8	18.8	2962	10	RNO6519	AJ006519 Rattus no
	34	492.8	18.8	3449	10	RNO309926	AJ309926 Rattus no
	35	491.2	18.7	3647	6	A87684	A87684 Sequence 4
	36	491.2	18.7	3647	6	AR168528	AR168528 Sequence
	37	491.2	18.7	3647	6	BD070034	BD070034 Mammal ne
	38	487.2	18.6	3658	6	AX683970	AX683970 Sequence
	39	443.4	16.9	3778	6	CQ717066	CQ717066 Sequence
	40	441.8	16.8	3785	9	HSU78181	U78181 Human sodiu
	41	440.2	16.8	1620	6	A87682	A87682 Sequence 2
	42	440.2	16.8	1620	6	AR168526	AR168526 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AX009297 2622 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9963081.
ACCESSION AX009297
VERSION AX009297.1 GI:9996624
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Akopian,A.N., England,S., Wood,J.N. and Chen,C.C.
TITLE Ion channels
JOURNAL Patent: WO 9963081-A 1 09-DEC-1999;
AKOPIAN ARMEN NORAKOVITCH (GB); UNIV LONDON (GB); ENGLAND STEVEN (GB); WOOD JOHN NICHOLAS (GB); CHEN CHIH CHENG (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:10116"
ORIGIN

Query Match 99.5%; Score 2609; DB 6; Length 2622;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 AGTTTAGAAGAGCAGCCGCTGCCACCACCACCACTCCGGAGGGCACCAGGGCTGCTGTCC 240
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